

|          |     |   |
|----------|-----|---|
| XM048113 | 1   | -----   |
| ANH401   | 1   | MAAVSLRLGDLVGKLRGYPPWPGKIVNPPKDLKKPRGKCFVKFFGTEDHAWIKVEQL                                 |
| AF326966 | 1   | MAAVSLRLGDLVGKLRGYPPWPGKIVNPPKDLKKPRGKCFVKFFGTEDHAWIKVEQL                                 |
| <br>     |     |   |
| XM048113 | 1   | -----   |
| ANH401   | 61  | KPYHAHKEMIKINKGKRFQQAVDAVEEFLRAKGKDQTSSHNSDDKNRRNSSEERSRP                                 |
| AF326966 | 61  | KPYHAHKEMIKINKGKRFQQAVDAVEEFLRAKGKDQTSSHNSDDKNRRNSSEERSRP                                 |
| <br>     |     |   |
| XM048113 | 1   | -----   |
| ANH401   | 121 | NSGDEKRKLSLSEGKVKKNMGEKKRVSSEGSERGSKSPKRAOEQSPRKGRGRPPKDEKD                               |
| AF326966 | 121 | NSGDEKRKLSLSEGKVKKNMGEKKRVSSEGSERGSKSPKRAOEQSPRKGRGRPPKDEKD                               |
| <br>     |     |   |
| XM048113 | 1   | -----   |
| ANH401   | 181 | LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK                              |
| AF326966 | 181 | LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK                              |
| <br>     |     |   |
| XM048113 | 1   | -----   |
| ANH401   | 241 | MGS GIVSNLLKMGHHTVTVWNRTA<br>ICEEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGMGSIVSNLLKMGHHTVTVWNRTA |
| AF326966 | 241 | ICEEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGMGSIVSNLLKMGHHTVTVWNRTA                              |
| <br>     |     |   |
| XM048113 | 24  | -----   |
| ANH401   | 301 | EKC DLF IQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPMSGVLOQGIRPGKCYVDM                          |
| AF326966 | 301 | EKC DLF IQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPMSGVLOQGIRPGKCYVDM                          |
| <br>     |     |   |
| XM048113 | 84  | -----   |
| ANH401   | 361 | STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM                              |
| AF326966 | 355 | STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM                              |
| <br>     |     |   |
| XM048113 | 144 | -----   |
| ANH401   | 421 | GKT SFFLGEVGNAAKMMILIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASI                            |
| AF326966 | 415 | GKT SFFLGEVGNAAKMMILIVNMVQGSFMATIAEGLTLAQVTGQSQQTLLDILNQGQLASI                            |
| <br>     |     |   |
| XM048113 | 204 | -----   |
| ANH401   | 481 | FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHP TPMAAAANEVYKRAKALDQS                             |
| AF326966 | 475 | FLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHP TPMAAAANEVYKRAKALDQS                             |
| <br>     |     |   |
| XM048113 | 264 | -----   |
| ANH401   | 541 | DNDMSAVYRAYIH   |
| AF326966 | 535 | DNDMSAVYRAYIH   |

Fig. 1